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## FIGURE 1

**A**

*AHASL1D*

WT

CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTCAAGGAC  
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGAC  
H V L P M I P N G G A F K D

**B**

*AHASL1B*

WT

CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTTAAGGAC  
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTTAAGGAC  
H V L P M I P N G G A F K D

**C**

*AHASL1A*

WT

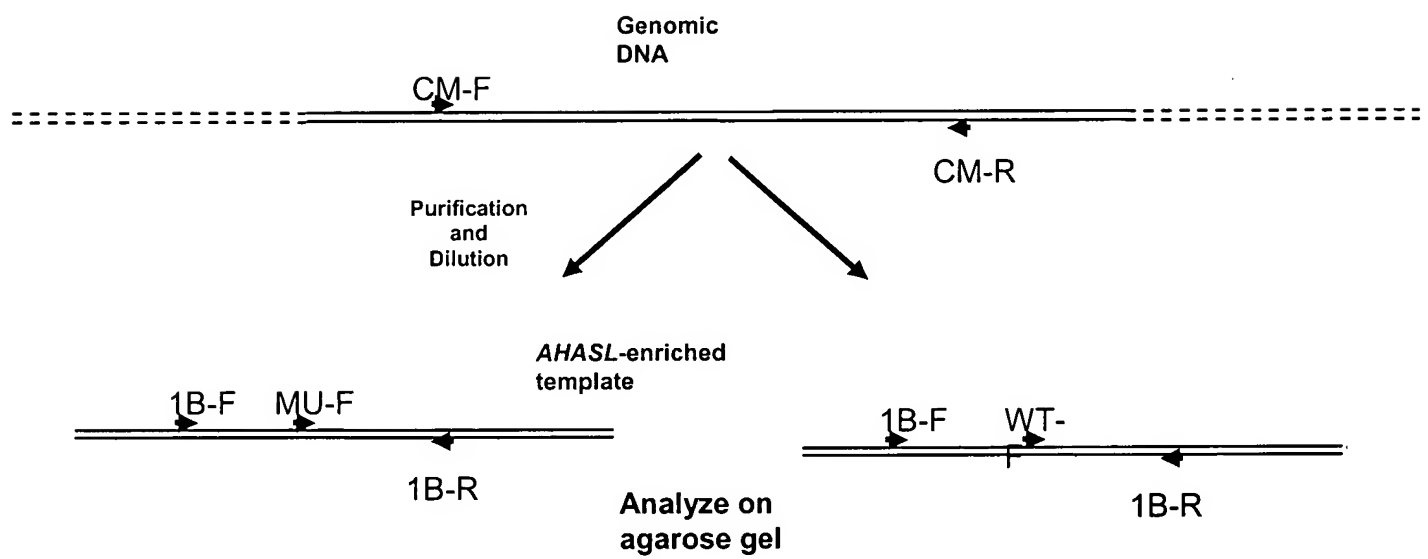
CACGTGCTGCCTATGATCCCAAGCGGTGGTGCTTTCAAGGAC  
H V L P M I P S G G A F K D

MUT

CACGTGCTGCCTATGATCCCAAACGGTGGTGCTTTCAAGGAC  
H V L P M I P N G G A F K D

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**FIGURE 2**



## FIGURE 3 (sheet 1 of 3)

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» AHASL1B (1251) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
» AHASL1D (945) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
» AHASL1A (1058) TTTGGTCCATGGCACAAGGAGTTGGATCAGCAGAAGAGGGAGTTTCCTCT
(1251)

» CM-F (1) CCGCCGCAATATGCTATCCA>>
» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
(1301) +

» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTGGG
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTGGG
(1351) + +

» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
(1401) +

» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTTGGGTTGCCAGCTG
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
(1451) + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
(1501)

» AHASL1B (1551) GGGGATGGTAGTTTCCTCATGAACATTAGGAGTTGGCGTTGATCCGTAT
» AHASL1D (1245) GGTGATGGTAGTTTCCTCATGAACATTAGGAGTTGGCGTTGATCCGCAT
» AHASL1A (1358) GGAGATGGTAGTTTCCTCATGAACATTAGGAGTTGGCATTGATCCGTAT
(1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
(1601) +

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## FIGURE 3 (sheet 2 of 3)

» AHASL1B	(1651)	TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1D	(1345)	TGGTGGTGCAAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1A	(1458)	TGGTGGTGCAATGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
	(1651)	+ +
» AHASL1B	(1701)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1D	(1395)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
» AHASL1A	(1508)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC
	(1701)	
» AHASL1B	(1751)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
» AHASL1D	(1445)	GATTGCTAAAGGATTCAACGTTCCAGCAGTTCGAGTGACGAAGAAGAGCG
» AHASL1A	(1558)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG
	(1751)	+ +
» AHASL1B	(1801)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1D	(1495)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
» AHASL1A	(1608)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG
	(1801)	
» AHASL1B	(1851)	TTGGATATCATTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1D	(1545)	TTGGATATCATAGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
» AHASL1A	(1658)	TTGGATATCATCGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG
	(1851)	+
» AHASL1B	(1901)	CGGTGGTGCTTTTAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1D	(1595)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
» AHASL1A	(1708)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT
	(1901)	+
» AHASL1B	(1951)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1D	(1645)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
» AHASL1A	(1758)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA
	(1951)	
» AHASL1B	(2001)	TGATACCTGCGTGTTGTATCAACTACTGGGGGTTCAACTGTGAACCATGC
» AHASL1D	(1695)	TGATGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGARCCATGC
» AHASL1A	(1808)	TGGTGCCCCGCGTGTTGTATCAACTACTAGGGGTTCAACTGTGAACCATGC
	(2001)	+ + + + +
» AHASL1B	(2051)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1D	(1745)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
» AHASL1A	(1858)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC
	(2051)	+

## FIGURE 3 (sheet 3 of 3)

» AHASL1B	(2101)	GAACCGTGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC	
» AHASL1D	(1795)	GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC	
» AHASL1A	(1908)	GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC	
	(2101)	+ + + + +	+
» AHASL1B	(2151)	ATAARATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGCACTTC	
» AHASL1D	(1845)	ATAARATRTCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC	
» AHASL1A	(1958)	ATAAAATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC	
« CM-R	(1)	<u>&lt;&lt;CATGCAAGTTTCTTGTCTA</u>	
	(2151)	+ +	+
» AHASL1B	(2201)	CATGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA	
» AHASL1D	(1895)	CATGCAGTAAAAAAAAAAAAAAAAAAAAAAAAA	
» AHASL1A	(2008)	CATGGAAAAAAAAAAAAAAAAAAAAAAAAA	
	(2201)	+ ++	

## FIGURE 4 (sheet 1 of 3)

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» AHASL1B (1301) AGGATTCAAGACTTTTGGTGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1D (995) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
» AHASL1A (1108) AGGATTCAAGACTTTTGGCGAGGCCATCCCGCCGCAATATGCTATCCAGG
(1301) +

» 1AD-F (1) GGGAGGCGATCATTG@CAG>>
» AHASL1B (1351) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACCGGTGTTGGG
» AHASL1D (1045) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCCACTGGTGTGGG
» AHASL1A (1158) TACTGGATGAGCTGACAAAAGGGGAGGCGATCATTGCTACTGGTGTGGG
(1351) + +

» 1B-F (1) GCGA
» AHASL1B (1401) CAGCATCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1D (1095) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
» AHASL1A (1208) CAGCACCAGATGTGGGCGGCTCAGTATTACACTTACAAGCGGCCACGGCA
(1401) +

» 1B-F (6) GTGGCTGTCTTCATC>>
» AHASL1B (1451) GTGGCTGTCTTCATCCGGTTTGGGTGCAATGGGATTTGGGTTGCCAGCTG
» AHASL1D (1145) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
» AHASL1A (1258) GTGGCTGTCTTCGTCTGGTTTGGGGGCAATGGGATTTGGGTTACCAGCTG
(1451) + + + +

» AHASL1B (1501) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1D (1195) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
» AHASL1A (1308) CAGCTGGCGCTGCTGTGGCCAACCCAGGTGTTACAGTTGTTGACATTGAT
(1501)

» AHASL1B (1551) GGGGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGTAT
» AHASL1D (1245) GGTGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCGTTGATCCGCAT
» AHASL1A (1358) GGAGATGGTAGTTTCCTCATGAACATTTCAGGAGTTGGCATTGATCCGTAT
(1551) + + +

» AHASL1B (1601) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1D (1295) TGAGAACCTCCCAGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
» AHASL1A (1408) TGAGAACCTCCCTGTGAAGGTGATGATATTGAACAACCAGCATCTGGGAA
(1601) +

« 1A-R (1)
» AHASL1B (1651) TGGTGGTGCAGTGGGAGGATAGGTTTTACAAGGCCAACCGGGCGCACACA
» AHASL1D (1345) TGGTGGTGCAGTGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
» AHASL1A (1458) TGGTGGTGCATGGGAGGATAGGTTTTACAAGGCCAATCGGGCGCACACA
(1651) + +

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## FIGURE 4 (sheet 2 of 3)

» AHASL1B	(1701)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
» AHASL1D	(1395)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
» AHASL1A	(1508)	TACCTTGGCAACCCAGAAAATGAGAGTGAGATATATCCAGATTTTGTGAC	
	(1701)		
» AHASL1B	(1751)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG	
» AHASL1D	(1445)	GATTGCTAAAGGATTCAACGTTCCAGCAGTTCGAGTGACGAAGAAGAGCG	
» AHASL1A	(1558)	GATTGCTAAAGGATTCAACGTTCCGGCAGTTCGTGTGACGAAGAAGAGCG	
	(1751)		+ +
» AHASL1B	(1801)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
» AHASL1D	(1495)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
» AHASL1A	(1608)	AAGTCACTGCAGCAATCAAGAAGATGCTTGAGACCCAGGGCCATACTTG	
	(1801)		
» WT-F	(1)		GTGCTGCCTATGATCCGAAG
» MU-F	(1)		CGTGCTGCCTATGATCCGAAC
» AHASL1B	(1851)	TTGGATATCATTGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
» AHASL1D	(1545)	TTGGATATCATAGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
» AHASL1A	(1658)	TTGGATATCATCGTCCCGCATCAGGAGCACGTGCTGCCTATGATCCCAAG	
	(1851)		+ + +
» AHASL1B	(1901)	CGGTGGTGCTTTTAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
» AHASL1D	(1595)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
» AHASL1A	(1708)	CGGTGGTGCTTTCAAGGACATGATCATGGAGGGTGATGGCAGGACCTCGT	
	(1901)		+
» AHASL1B	(1951)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
» AHASL1D	(1645)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
» AHASL1A	(1758)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
Contig 1	(1951)	ACTGAAATTTTCGACCTACAAGACCTACAAGTGTGACATGCGCAATCAGCA	
	(1951)		
» AHASL1B	(2001)	TGATACCTGCGTGTTGTATCAACTACTGGGGGTTCAACTGTGAACCATGC	
» AHASL1D	(1695)	TGATGCCC GCGTGTTGTATCAACTACTAGGGGTTCAACTGTGARCCATGC	
» AHASL1A	(1808)	TGGTGCCC GCGTGTTGTATCAACTACTAGGGGTTCAACTGTGAACCATGC	
« 1B-R	(1)	<b>&lt;&lt;ACCTGCGTGTTGTATCAACTACT</b>	
	(2001)	+ + +	+ +
» AHASL1B	(2051)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
» AHASL1D	(1745)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
» AHASL1A	(1858)	GTTTTCTAGTTTGCTTGTTTCATTTCATATAAGCTTGTGTTACTTAGTTCC	
	(2051)		+



## FIGURE 4 (sheet 3 of 3)

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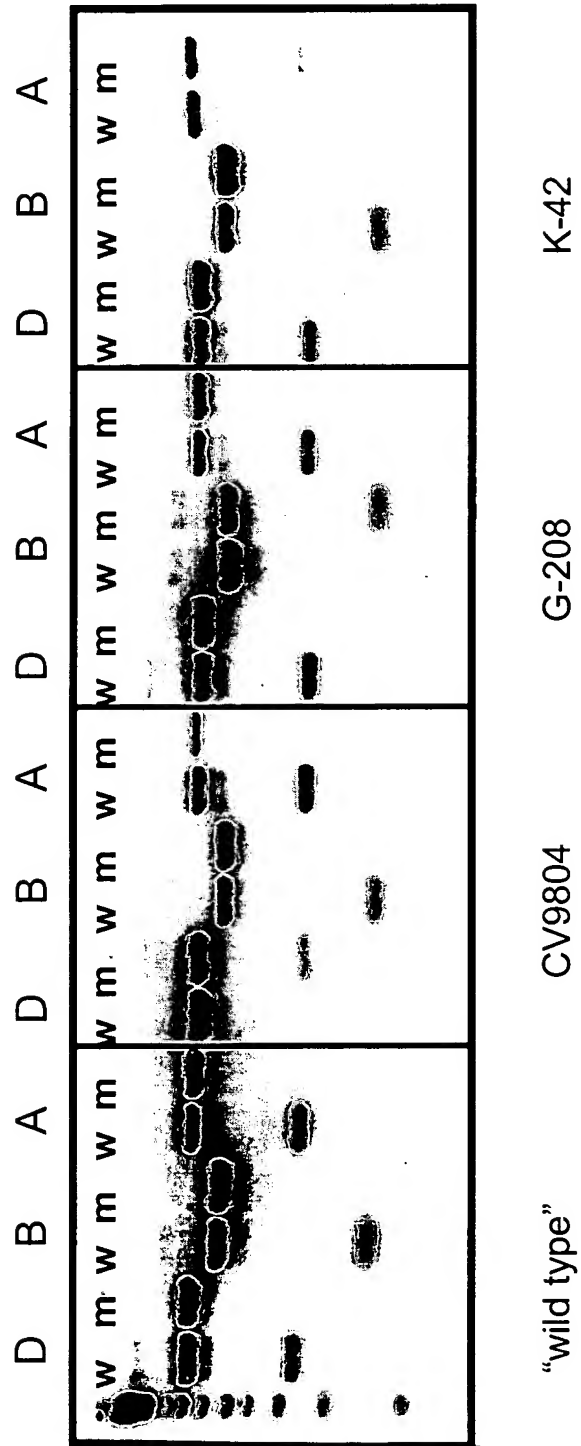
» AHASL1B (2101) GAACCGTGTAGTTTTGTAGTCTCTGTTCTCTTTTGTAGGGAYGTGCTGTC
» AHASL1D (1795) GAACCCTGTAGTTTTGTAGTCTATGTTCTCTTTTGTAGGGATGTGCTGTC
» AHASL1A (1908) GAACCCTGTAGCTTTGTAGTCTATGCTATCTTTTGTAGGGATGTGCTGTC
    « 1D-R (1)                                     <<ATCTTCTCTTTTGTAGGGATGTC
    « 1A-R (1)                                     <<CTATCTTTTGTAGGGATGTGCTGT
    (2101)          +      +      + ++ +      +

» AHASL1B (2151) ATAARATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGCACTTC
» AHASL1D (1845) ATAARATRTCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC
» AHASL1A (1958) ATAAAATATCATGCAAGTTTCTTGTCTACATATCAATAATAAGTACTTC
    (2151)          +      +      +

» AHASL1B (2201) CATGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1D (1895) CATGCAGTAAAAAAAAAAAAAAAAAAAAAAAAA
» AHASL1A (2008) CATGGAAAAAAAAAAAAAAAAAAAAAAAAA
Contig 1 (2201) CATGSARHAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 5



**FIGURE 6**

	Hexaploid L1D	Hexaploid L1B	Hexaploid L1A	Tetraploid L1B	Tetraploid L1A
Hexaploid L1D	100%	97.8%	98.2%	97.4%	97.8%
Hexaploid L1B		100%	97.7%	99.4%	97.3%
Hexaploid L1A			100%	97.3%	99.6%
Tetraploid L1B				100%	97.6%
Tetraploid L1A					100%